FIG. 1A

```
gtgttgctcc actgtcagtc ctccagagcc tcaagagatc tttgggccat atcagctttc 60

tttccaaaat gaacacaccc aggggcagga aagaatgctc tttccttggt cattaagggg 120

cctgggagtc ctggaccagc ttttcatgca gctagaccac ttacatgcaa ctagagcctt 180

gactttgaaa cgagggacaa aagcatctct tgctaaaggt aacttctgct gcttagaacc 240

cagcctcctc accaccatct gatctatctt gttctcttca caaaaggctc tgaagacatc 300

atg aac cca caa cgg gag gca gca ccc aaa tcc tat gct att cgt gat   348
Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
  1               5                  10                  15

tct cga cag atg gtg tgg gtc ctg agt gga aat tct tta ata gca gct   396
Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
             20                  25                  30

cct ctt agc cgc agc att aag cct gtc act ctt cat tta ata gcc tgt   444
Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
         35                  40                  45

aga gac aca gaa ttc agt gac aag gaa aag ggt aat atg gtt tac ctg   492
Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
     50                  55                  60

gga atc aag gga aaa gat ctc tgt ctc ttc tgt gca gaa att cag ggc   540
Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
 65                  70                  75                  80

aag cct act ttg cag ctt aag gaa aaa aat atc atg gac ctg tat gtg   588
Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
                 85                  90                  95

gag aag aaa gca cag aag ccc ttt ctc ttt ttc cac aat aaa gaa ggc   636
Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
            100                 105                 110

tcc act tct gtc ttt cag tca gtc tct tac cct ggc tgg ttc ata gcc   684
Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
        115                 120                 125

acc tcc acc aca tca gga cag ccc atc ttt ctc acc aag gag aga ggc   732
Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
    130                 135                 140

ata act aat aac act aac ttc tac tta gat tct gtg gaa taa           774
Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
145                 150                 155

atccagccta ggctgtgggt ggctggttcc aggatagaga atcaagctgt cagagtcatc 834

ttaacagatc attatgcgac tgagttcact agcagttcag cccatccata gcttacctca 894
```

FIG. 1B

ttcttactat ccaaaagcca cctcctcctc caaacatcca tttctgtacc aagaccctca 954

ctcgaatgtc actatcccaa gatgaaacct aaaaatcact ttccattctt tcttgatctt 1014

accccaccat ccactcagct gccatgccca gtttagttaa ccccccaaat gctgcttcat 1074

gcaaccttcc attcctattc cttttgccaa cccatgatgt agagatgtgg attcatgaca 1134

ttttgttcat acaacttctt caataaaaca ttataatatg tgccccaaag ataaagctga 1194

agaatgagat gaatgtgaaa ttaaaggttt gcatgtcttc ctaatcctaa 1244

FIG. 2

```
                1                                                   50
  IL-1_delta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~MNPQ REAAPKSYAI RDSRQMVWVL
    IL-1ra-L ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~MNPQ REAAPKSYAI RDSRQMVWVL
IL-1_epsilon ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~MEKAL KIDTPQQGSI QDINHRVWVL
  IL-1ra_sec MEICRGLRSH LITLLLFLFH SETICRPSGR KSSKMQAFRI WDVNQKTFYL
   IL-1_beta ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ APVRSLNCTL RDSQQKSLVM
   consensus ---------- ---------- ------MNPQ -EAAP-SYAI RDS-Q-VWVL

                51                                                  100
  IL-1_delta SG.NSLIAAP LSRSIKPVTL HLIACRDTEF SDKEKGNMVY LGIKGKDLCL
    IL-1ra-L SG.NSLIAAP LSRSIKPVTL HLIACRDTEF SDKEKGNMVY LGIKGKDLCL
IL-1_epsilon QD.QTLIAVP RKDRMSPVTI ALISCRHVET LEKDRGNPIY LGLNGLNLCL
  IL-1ra_sec RN.NQLVAGY LQ...GP.NV NLEEKIDVVP IEP...HALF LGIHGGKMCL
   IL-1_beta SGPYELKALH LQGQDMEQQV .VFSMSFVQG EESNDKIPVA LGLKEKNLYL
   consensus SG-NSLIAAP L-RSIKPVT- HLI-CRDVEF SEKEKGN-VY LGIKGK-LCL

                101                                                 150
  IL-1_delta FCAEIQGKPT LQLKLQGSQD .NIGKDTCWK LVGIHTCINL DVRESCFMG.
 IL-1ra-LFCAEIQGKPT LQLKEKNIMD LYVEKKAQKP FLFFH...NK EGSTSVFQSV
IL-1_epsilon MCAKVGDQPT LQLKEKDIMD LYNQPEPVKS FLFYH...SQ SGRNSTFESV
  IL-1ra_sec SCVKSGDETR LQLEAVNITD LSENRKQDKR FAFIR...SD SGPTTSFESA
   IL-1_beta SCVLKDDKPT LQLESVDPKN .YPKKKMEKR FVFNKIEINN KLE...FESA
   consensus -CA-I-DKPT LQLKE--IMD LY--KK--KR F-FIH--IN- SGRTS-FES-

                151                                             193
  IL-1_delta TLDQWGIGVG RKKWKSSFQH HHLRKKDKDF SSMRTNIGMP GRM
    IL-1ra-L SYPGWFIATS TTSGQPIF.. ...LTKERGI TN.NTNFYLD SVE
IL-1_epsilon AFPGWFIAVS SEGGCPLILT QELGKANTTD FGLTMLF~~~ ~~~
  IL-1ra_sec ACPGWFLCTA MEADQPVSLT N...MPDEGV MVTKFYFQED E~~
   IL-1_beta QFPNWYISTS QAENMPVFLG GTKGGQDITD FTMQFVSS~~ ~~~
   consensus AFPGWFIATS -E-GQPVFLT --LGKKD--D F-M--NF--D ---
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